

Composite Collection

At ICRISAT genebank, as part of the Generation Challenge Program (GCP) under project: GCP. (SP1)2006-31, which aims to create a public platform that will use molecular methods to unlock genetic diversity and put it to use for the world's poorest farmers, developed a global composite collection of pearl millet. The composite collection consist 1021 accessions representing the world collection of 21,594 pearl millet germplasm accessions held at ICRISAT genebank, ecologically, taxonomically and phenotypically (Table 3). The composite collection include accessions of core collection, accessions tolerant/resistant and susceptible to different abiotic and biotic stresses, trait specific germplasm, wild relatives and contributions from crop improvement scientists in ICRISAT and NARS. Biological status of composite collection reveal 704 landraces, 182 advanced breeding lines, and 60 accessions from the seven wild relatives from ICRISAT genebank and 75 advanced lines from crop improvement scientists in ICRISAT and Indian NARS. Geographically, 441 accessions belongs to Asia, 359 to West Africa, 161 to Southern Africa, 42 to Eastern Africa, 12 to Central Africa, five to America's, and one to Europe. Considering the heterogeneity of the accessions, 15 plants per accession were selected for DNA extraction, and the DNA was pooled to capture within accession variation.

Genetic Structure of Composite Collection

Nineteen SSR markers (Allouis et al. 2001; Qi et al. 2001, 2004; Senthilvel et al. 2004) data on 1021 accessions were analyzed using PowerMarker V3.0 (Liu and Muse. 2005) and DARwin 5.0 version (Perrier et al. 2003). This composite collection showed a total of 230 alleles, averaged 12 alleles per locus and 102 of them were rare alleles at 1%. The accessions were highly heterogeneous and up to 7 alleles were detected per locus. The accessions were grouped by geographical locations but not by biological status. Only seven alleles were unique to wild species whereas none were found in landraces. The released cultivars and advanced lines scattered across different groups (Figure 1). The allelic data of 19 SSR loci for 1021 accessions will be made available to the GCP central repository.